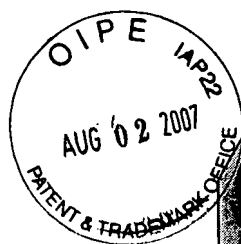


EXHIBIT A**FIGURE 1**

5' to 3'

T7 promoter

5' 601 TAAAACGACG GCCAGTGAGC GCGCGTAATA CGACTCACTA TAGGGCGAAT
 3' ATTTTGCTGC CGGTCACTCG CCGGCATTAT GCTGAGTGAT ATCGGCGTTA

5' GGGCGAAU

1. Hae III cleavage of plasmid plus T3 polymerase transcription
2. Pvu II cleavage of plasmid plus T7 polymerase transcription

5' 651 TGGAGCTCCA CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG
 3' ACCTCGAGGT GCGGCCACCG CCGCGGAGAT CTTGATCATT TAGGGGGCCCC

5' UGGUGCUCCA CCGCGGUGGC GGCCGCUCUA GAACUAGUGG AUCCCCCGGG

5' 701 CTGCAGGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC TCGAGGGGGG
 3' GACGTTCTTA AGCTATAGTT CGAATAGCTA TGGCAGCTGG AGTCCCCCCC

5' CUGCAGGAU UCGAUAUCAA GCUUAUCGAU ACCGUCGACC UCGAGGGGGG

Hae III

5' 751 GCGCGGTACC CAGCTTTTGT TCCGTTTAGT GAGGGTTAAT TCGCGGCTTG
 3' CCGGCGATGG GTCGAAACA AGGAAATCA CTCCCAATTA ACGCGCGAAC

3' GGGCAUGG GUCAAACA AGGG 5'
 5' GCCCGGUACC CAGCUUUUGU UCCCUUAGU GAGGGUAAU

T3 promoter

5' to 3'

EXHIBIT A

FIGURE 2A

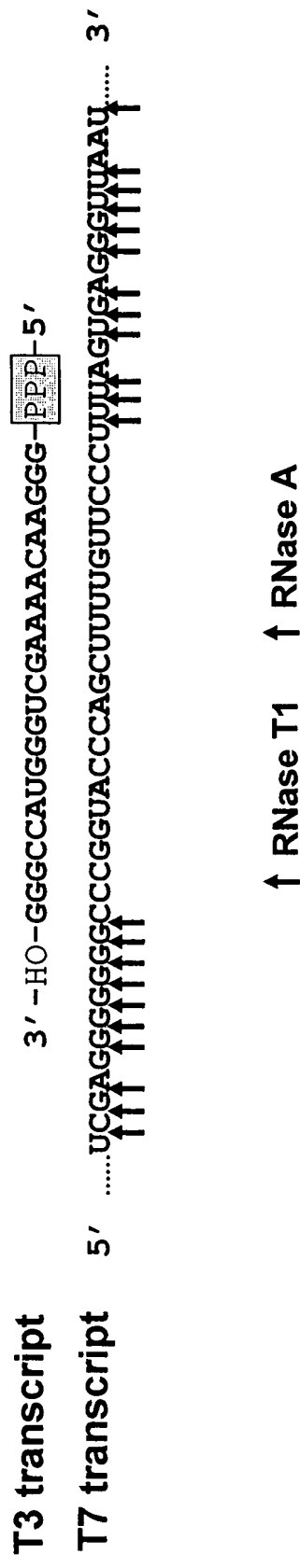


FIGURE 2B

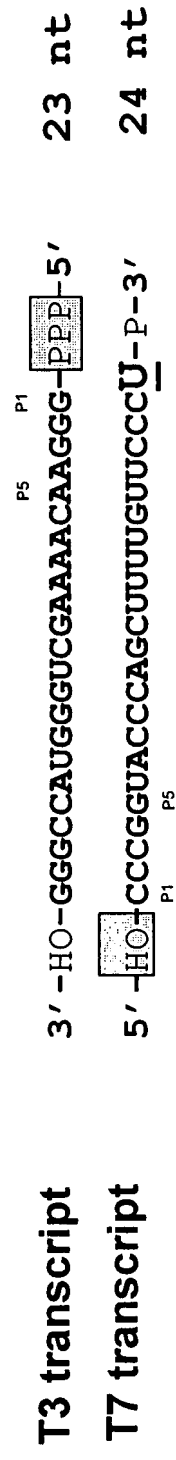


EXHIBIT A

Transcript 3'end
Heterogeneity
(Size Range (nt))

Yes
(100-104+)

Yes
(81-85+)

Yes
(63-67+)

Yes
(51-55+)

Yes
(36-40+)

Yes
(30-34+)

Template 5' End
(top strand = template strand)

3' ←----- 5'
104 100
5' -GGCCGCTCTAG-3'
CGAGATC-5'

3' ←----- 5'
85 81
5' -GATCCCCCGGG-3'
CGGGCCC-5'

3' ←----- 5'
67 63
5' -AATTCGAATTC-3'
TTAAGCT-5'

3' ←----- 5'
55 51
5' -AGCTTATCGAT-3'
ATAGCTA-5'

3' ←----- 5'
40 36
5' -TCGACCTCGAG-3'
GGAGCTC-5'

3' ←----- 5'
34 30
5' -TCGAGGGGGGG-3'
CCCCCCC-5'

FIGURE 3A

Restriction Digest
(+HaeIII)

Eag I
↓
CGGCCG
GCCGGC

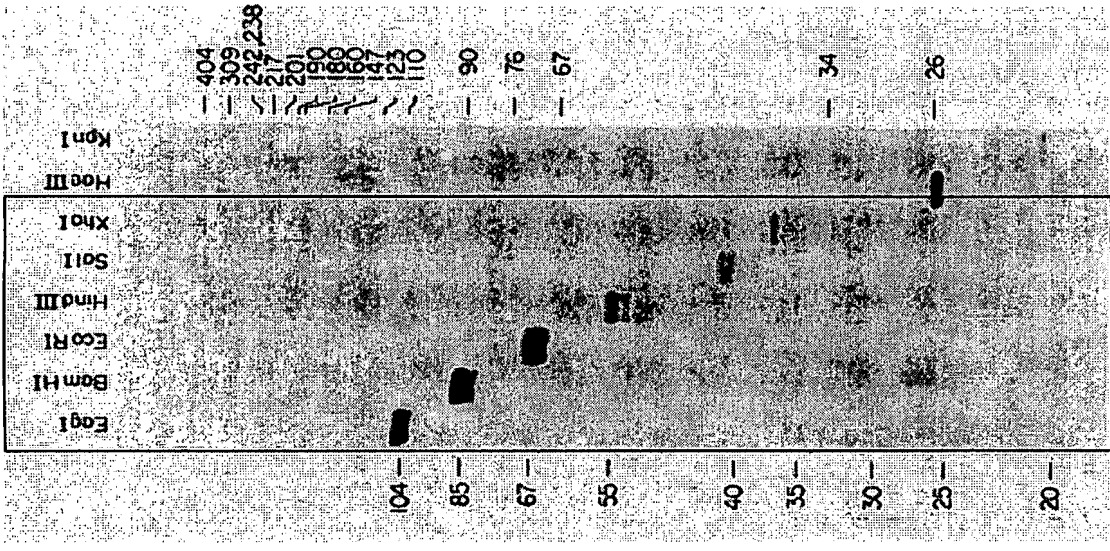
BamH1
↓
GGATCC
CCTAGC

EcoR1
↓
GAATTC
CCTAGC

HindIII
↓
AAGCTT
TTCGAA

Sal I
↓
GTCGAC
CAGCTC

Xho I
↓
CTCGAG
GAGCTC



----- "Run-On" T3 Transcription
----- Defined T3 Transcription
100 G No. of bases from 3' end

EXHIBIT A

FIGURE 3B

